Leffers

BIOTEC. /LOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/430,590B

Source: 1636

Date Processed by STIC: 11/13/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION

SERIAL NUMBER: 09/430,598

TECH CENTER 1600/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid-number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: **This sequence is intentionally skipped** Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	**Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

1636

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/430,590B

DATE: 11/13/2000
TIME: 13:13:56

Does Not Comply
Corrected Diskette Needed

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Output Set: N:\CRF3\11132000\I430590B.raw

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  4       POULTER et al.
  6 <120> TITLE OF INVENTION: UNUSUAL RETROTRANSPOSON FROM THE YEAST CANDIDA ALBICANS
  8 <130> FILE REFERENCE: 674521-2001.1
 10 <140> CURRENT APPLICATION NUMBER: 09/430,590B
 11 <141> CURRENT FILING DATE: 1999-10-29
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 30 ttgaagcaaa agaaaagttt ggcatcaagc tagatattta tatatgtata tgattagacc 180
 31 aacataaaac tagacgtcca aatatttatt tatttattta ttgatatata ttcttattta 240
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RAW SEQUENCE LISTING DATE: 11/13/2000
PATENT APPLICATION: US/09/430,590B TIME: 13:13:56

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RAW SEQUENCE LISTING DATE: 11/13/2000
PATENT APPLICATION: US/09/430,590B TIME: 13:13:56

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RAW SEQUENCE LISTING DATE: 11/13/2000
PATENT APPLICATION: US/09/430,590B TIME: 13:13:56

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RAW SEQUENCE LISTING DATE: 11/13/2000
PATENT APPLICATION: US/09/430,590B TIME: 13:13:56

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229 <223> OTHER INFORMATION: N stands for any nucleotide
231 <400> SEQUENCE: 6
232 gtgtagatgc aataggtgta tgaaatgtat ctagattata tcatgaagcc cttgccaata 60
233 aaatctagcc aaaaatttgt gtactgcaat tgttcgctat agagagatat cctagccgga 120
234 atgcacgaca atcctgagac ggaagtcgat cgtcgatgcc catggtgcgt ggtgaaaaat 180
235 tntcttagaa aatttgttct ttccttcaac tgcttttaag agaagggagg ttcaagtggt 240
236 ttaagtacga cggtcacaaa gattgcggct tatgaggccc gaactgagtt gaaatacaaa 300
237 atcaagatat aattatatac cttacttgtc tatattgttt tataatacat tcttcagata 360
238 tttaaatttc tgtgtatcat cctataaaac agagatacat tcagtacatt tagtatactg 420
239 agtgaactgg tacctgtgac attcaagata actgtttcgc gcacgctggc agacgaacag 480
240 caattctgta attgtcgtag agtagcaaca aatcttcccg atgattggta cttgtgttag 540
241 tctacacgac atgtgttttg gtacacttga actgtatgtc caagaatgga aacatatgcg 600
242 ggaaggacgc gaaagatgag tttggtatag aagggataag aactgtaaaa tatattatgt 660
243 agttatatat tttaattatg ggaaattgag tgtttattct gttcaacaag tttcaaccgt 720
244 agagattaca tttaaagtct gtggtcgaaa tccacaagat acagcaaatt catgaattca 780
245 cctatttaaa tcaagtttac caagcaccat tgcctagaac ttgccatatc atcaattaag 840
246 tcagacatta ctaatttgag caaagctttt agcttaatgg gccaactaat ttaagtcgaa 900
247 ttggtaatgc aatctgttct tcatttgagt cgcttgctac ggctccatga cacatccatt 960
248 tgattgtttt aattcgagca attatccacc ataactctca gtaatatcat taacagtttt 1020
249 acgcttaata agcatagaaa gttgtatgaa gttgtctcct aggtatgcta gagagatttg 1080
250 tatatacgac cagtaaagag tgtgatgagg tgtttactgt agggtaaatt gcaattgact 1140
251 tgagttgata gcggttatta caaaagtata gattcaacaa attaagacaa gtaccaaacg 1200
252 ataggccgaa tgtgacttat accgttgaag ttcaagcgtt tttaacaaat agaaatgtga 1260
253 gattaatgag ttcgacaaat gttttactag atactattaa tttcgatgta ctatataagt 1320
254 ttaaccagct ataaccggca gagcagactt cctgaaactc aaattggttg tgtttggact 1380
255 tgagttacac cacaaagttt gacaatcgtg aggacatagc aacctatcaa gccactca 1438
258 <210> SEQ ID NO: 7
259 <211> LENGTH: 1304
260 <212> TYPE: DNA
261 <213> ORGANISM: Candida albicans
263 <400> SEQUENCE: 7
264 tgaagatctg gctttggcca aagtatcagc tgcattagat actgtcattg gcattggctt 60
265 gaacccactg gctgtggatg taactgtgga gccaaaagct cgtaaagctt tggcgttcat 120
266 ggagaaaaat cttttaacag acattgtata aacgttgaag attaaagaaa aaaaaaacag 180
267 aaagattacg aataatttgt ttttaattgg tgggtatgag gtgttgcgca gtcgactcaa 240
268 caattctctt ttggtgcaca aagttggttt tatggtcaac aattacggag tactgtctgt 300
269 agtgatgttg aatctaagac ggaaatgcct cctttacatt tgtttctatt ctcttaaaat 360
270 acatattcaa ttgtgtgttt taattgaaaa tttgttcatc ttcatctgat gattgtgtaa 420
271 tctttgcggg gggggggcgt gtcatgaacc aatctctttg agtcatagga cgagtcatcc 480
272 tattgtgact catggctcat cttactctct tactaatctc ttacttcatc tgtttactat 540
273 aaatatgtct actactcctc tattttatta cctcgtttac tatttttatt caatatatga 600

Partial listing of Sequence 16

<210> 16
<211> 6140
<212> DNA
<213> Candida albicans

<400> 16
agtaaaaaaa gaagaaaaaa aagctaaaat tgggacaata tgctaagtat atatagggga 60
agacgtcgaa cagcaaccac ggaaaaataa tagtgattgt ctttatccgt tattggctgg 120
atggcgacgc cacaacctga aatttggttc caactgttga ggatgattta tgtttgtgat 180
tagaactaaa atcattcgag aaaaaaggaa taggagagaa ccaactttag tcgtgtaaaa 240
agtaacatct gccaattata aactatacgt agtccaaata atttacggta tatttctgta 300
ccccttcttg gcaatatcac aagaatatca taatgttcat gaaccctctt tgaacacgta 360
gacaagtaaa cccaatgagg gggcagtgtt ctattcttgt aaactgcgca ccaaaaacgg 420
ggcttaaaaa ataagttatg aaaactataa ataaccatga aaatcaccct actcccttcc 480
tcccttcctt ccttccttcc ttccttttct cttttcctct acccacacta ctcacaatgt 540
tcggtatttt tgaggaaaac tacgattctg tttacaaagg caaccacgaa gccaagttct 600
ctcacgaagc agttgctggt gctgcttcat ttgctgctgt caagttgttt gaagatagac 660
aaagaagaga agggaaacca gttagtcacg cctttgctaa agaagcttta gctgctattg 720
ctggtggaga agtcgacaaa ttatttgaaa ccaaagggtt ggactatttg gatagagaga 780
gacttagaga tcaagctatc aacaacgctc aaagaggtta cgacgaccat tacggtcaac 840
acgaagaatg gtctccagaa cacagaccac cttttgacta ccaaagatat taagtagaaa 900
ctgtgtagtg aatttacaat ttttttgaca agaattaact taaacctcgt ttttaggttt 960
tgtgcggctt ttgtcaattg acgatcctgt atatttcgtc ataattcaca cattcttaaa 1020
attatgcaca catccttgaa atgtgttaat attcccaaca ttatcaatta tatgtgttca 1080
gaattggttg caaagttatc aactcaattc acgctatata aaccttacaa attctctaca 1140
tttttatatt tttttatatt ggcttttctt ttagaatcaa tcaatacttt ttttatcatt 1200
tagatacatc tttcatctat taatagatta tctttctata tatcaaaaca cgacacagtc 1260
acgtgccaaa aaggatataa gaaggaactt cagaaaatta attttctgat tatactactt 1320
actagatttc ataaagtcaa tatctgattg atacaacttg gttcattatt cataaaactt 1380
tacaactaat tnnacaagna aaccnnacaa aaaaatccna atnaaataat cnnnnnaata 1440
ttataattaa ttaattacaa aaaaaaacaa aaaaatacac acacacatac acacacacaa 1500
aatcttgttg caaaaaaaaa aaaataataa taatataata agaattaatt aacaatgtcg 1560
tttccacgga cacattcacc aagaccatct ggttcacgag aacaggaaga tctcacactg 1620
atgattaaag cttttagaga ttcaatggaa gctaagcttg acttgcattc gcagaagctt 1680
actgctttgg tagcaaacat tcccagaacg gacgaagggt ttgaagattt atcacaaagg 1740
atcactgttc ttaaaaatca tcaaaaagca tttttgccca aacaagaaaa agaaatcgga 1800
agtcttctcc acagacaaag agaggaagaa ggtgatatta aggatttcaa aacagtcgtt 1860
ggtgaagaaa aagaagaatt gcaccaggtt gaagatttcg ttttaaaaga tcaagaagaa 1920
ttacgaaacg tcgaaaagaa agttttgaaa gaagaagaag aattgcaaaa agtggaagag 1980
tcaatggaaa aggaaaaaca agagttatac caggttgaag actttatttt gcaaagagat 2040
gagacggtaa agaaacttgg agaaagcaat caatctcaac aggaaccata tacacctgca 2100
acttctggtt cggatcagag attcagatct caacaaccta acattggaaa taccttagcg 2160
caggatctag cattaattcc aaaattagat ctggaaattt gcaaaattgc agtcaaatat 2220
ccaaaattat ttgaaacaaa attaagacca ccaccaccca gagactttca atataaaatt 2280
caactcacag accacactca aatttattca aaaccatata aatgcaatca agaagaacaa 2340
gctctcatca aggatttcat caatgaaaaa ttagaagcag gcgttttggt accagctcca 2400
attgatgctt ggttacaccc aatatttcca atcagaaaaa ccaatgccaa ccaatcctcc 2460
accaaaatag cagttgattt aagacgtctc aataaggtca cagtacgaat gtacacttat 2520
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atttcaacat ccgaggggaa ttattgcttt acaactttac cgtttggagc aatcaattcc 2700
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tacatggatg atatcctcat ccatactaaa accttacatg accacatgtc attactcagg 2820
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ttaacaacaa aaatcaattt cttagggtac agcattcaag cgaacaaaat atcaccagat 2940
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gcatttgtca atttcagcaa ccactttcgc atcttcatcc cagaaatagc aaaatttact 3060

See item 10 on Error Summary Sheet

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 11/13/2000
PATENT APPLICATION: US/09/430,590B TIME: 13:13:57

Input Set : A:\Poulter1.app
Output Set: N:\CRF3\11132000\I430590B.raw

L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:873 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:873 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:873 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:873 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:873 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:1367 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1367 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:1381 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
M:340 Repeated in SeqNo=20
L:1384 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1385 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
L:1433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1634 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:1634 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1634 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1634 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1634 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1635 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:1635 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25

VERIFICATION SUMMARY DATE: 11/13/2000
PATENT APPLICATION: US/09/430,590B TIME: 13:13:57

Input Set : A:\Poulter1.app
Output Set: N:\CRF3\11132000\I430590B.raw

L:1635 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1635 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:1696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1697 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1728 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1728 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:4009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72